

10	20	30	40	50	60	70
GATCACTGGG ACCAGGCGT GATCTCTATG CCCGAGTCTC AACCTCAAC TGTCACCCCA AGGCACTTGG						
80	90	100	110	120	130	140
GACGTCTTGG ACAGACCGAG TCCCGGGAAG CCCAGCACT GCCGTGCCA CACTGCCCTG AGCCCAAATG						
150	160	171	180	189	198	
GGGGAGTGAG AGGCCATAGC TGTCTGGC ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG						
MET Gly Leu Ser Thr Val Pro Asp Leu Leu						
207	216	225	234	243	252	
CTG CCG CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT						
Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile						
261	270	279	288	297	306	
GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC CAA						
Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln						
315	324	333	342	351	360	
GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC AAG TGC CAC AAA						
Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys						
369	378	387	396	405	414	
GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG						
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg						
423	432	441	450	459	468	
GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC						
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu						
477	486	495	504	513	522	
AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA						
Ser Cys Ser Lys Cys Arg Lys Glu MET Gly Gln Val Glu Ile Ser Ser Cys Thr						
531	540	549	558	567	576	
GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG						
Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp						
585	594	603	612	621	630	
AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG						
Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val						
639	648	657	666	675	684	
CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC						
His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe						

Fig. 21

693	702	711	720	729	738
TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG					
Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu					
747	756	765	774	783	792
TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA					
Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser					
801	810	819	828	837	846
GGC ACC ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA TCC					
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser					
855	864	873	882	891	900
CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG TCC AAG CTC TAC					
Leu Leu Phe Ile Gly Leu MET Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr					
909	918	927	936	945	954
TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA GAG GGG GAG CTT GAA GGA ACT					
Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr					
963	972	981	990	999	1008
ACT ACT AAG CCC CTG GCC CCA AAC CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC					
Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr					
1017	1026	1035	1044	1053	1062
CCC ACC CTG GGC TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC					
Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr					
1071	1080	1089	1098	1107	1116
TAT ACC CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA					
Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro					
1125	1134	1143	1152	1161	1170
CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC CCC ATC					
Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile					
1179	1188	1197	1206	1215	1224
CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC CTA GAC					
Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp					
1233	1242	1251	1260	1269	1278
ACT GAT GAC CCC GCG ACG CTG TAC GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC					
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg					
1287	1296	1305	1314	1323	1332
TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG AGC GAC CAC GAG ATC GAT CGG CTG					
Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu					

Fig. 21

1341	1350	1359	1368	1377	1386
GAG CTG CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA TAC AGC ATG CTG GCG ACC					
Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser MET Leu Ala Thr					
1395	1404	1413	1422	1431	1440
TGG AGG CGG CGC ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG CTG GGA CGC GTG					
Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg Val					
1449	1458	1467	1476	1485	1494
CTC CGC GAC ATG GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC					
Leu Arg Asp MET Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys					
1503	1512	1521	1530	1546	1556
GGC CCC GGC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGA GGCTGCGCCC CTGCGGGCAG					
Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg					
1566	1576	1586	1596	1606	1626
CTCTAAGGAC CGTCCTGCGA GATCGCCTTC CAACCCCACT TTTTCTGGA AAGGAGGGGT CCTGCAGGGG					
1636	1646	1656	1666	1676	1696
CAAGCAGGAG CTAGCAGCCG CCTACTTGGT GCTAACCCTT CGATGTACAT AGCTTTTCTC AGCTGCCTGC					
1706	1716	1726	1736	1746	1766
GCGCCGCCGA CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTGGGC TCAAGAGCCT GAGTGGGTGG					
1776	1786	1796	1806	1816	1836
TTTGCGAGGA TGAGGGACGC TATGCCTCAT GCCCGTTTTG GGTGTCTCA CCAGCAAGGC TGCTCGGGGG					
1846	1856	1866	1876	1886	1906
CCCCTGGTTC GTCCCTGAGC CTTTTTCACA GTGCATAAGC AGTTTTTTTT GTTTTTGTTT TGTGTTT					
1916	1926	1936	1946	1956	1976
TGTTTTTAAA TCAATCATGT TACACTAATA GAAACTTGGC ACTCCTGTGC CCTCTGCCTG GACAAGCACA					
1986	1996	2006	2016	2026	2046
TAGCAAGCTG AACTGTCTA AGGCAGGGGC GAGCACGGAA CAATGGGGCC TTCAGCTGGA GCTGTGGACT					
2056	2066	2076	2086		
TTTGTACATA CACTAAAATT CTGAAGTTAA AGCTCAAAAA AA					

FIG. 21